



COMMONWEALTH of VIRGINIA

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TO: Oskar Zaborsky
Victor McKusick

FROM: Paul B. Ferrara

SUBJECT: Sign-off on Draft Report

While I am generally in agreement that the majority of this report (summary, chapters 1-2, and 4-7) "satisfactorily represents the viewpoint of the committee", I am not ready to ascribe that condition to Chapter 3, Statistical Basis for Interpretation.

In view of our many discussions, presentations, and extensive information supplied to our committee, the recent published writings of some members of our committee, and through the remarks of the reviewers, I simply am not convinced that, in its current form, Chapter 3 demonstrates a balanced (as we contend on line 5; p. 3-33), consistent and objective consideration of this subject.

Stated succinctly, I think that the recommendations contained in Chapter 3 will lead to our understatement of the power of this technology and goes beyond a simply conservative approach. Lines 14-15 of p. 3-3, indicate that "any loss of power can be offset by studying additional loci". However, if forensic scientists are to be limited to use of the empirical counting method (1/N) for reporting purposes then how will the use of additional loci change this number? In fact, if a population database of 1000 genotypes is used, only one or two loci might be necessary to differentiate among all 1000 genotypes in the database and thereby mitigate the need to run more loci. How do we reconcile recommending statistical reporting of less than 1/1000 against our qualitative statement in the Chapter (lines 1-3, p. 3-37) that "a match occurring at each of four loci by chance is probably quite rare"?



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As I read this chapter and anticipate the effect of its use in criminal trials, I interpret that forensic laboratories would have to use the empirical counting method until the use of the multiplication rule is supported by the results of the population substructure study we describe on p 3-21. From a practical standpoint, that means that for a period extending from the issuance of this report until the publication of the results of the substructure study, reporting of statistical inferences of our data will be limited to the counting method; this could mean 1-2 years of reporting results grossly understating the significance of those results.

If I thought that that recommendation represented the majority opinion of the relevant scientific community, I could sign-off on this report. But as I have said all along, I am still not convinced the National Academy of Science could defend the basis of that conclusion. It would seem instead that the committee has selectively ignored much recently published material germane to this issue; for example, on line 20-23 of p. 3-9, we reference only five "studies concerning the population substructure of VNTR markers" when many more have been made available to the committee. The series of letters to the editor (Ann J. Hum, Genet. 49:891-903, 1991) and the responses to Hartl and Lewontin in the Crime Lab Digest (18:3), July 1991 distributed to the members of this committee with this draft are given only lip-service in Chapter 3 as are the comments of reviewers R-1, R-2, R-4, R-5, and R-6. It seems instead that the tone of Chapter 3 reflects a singular point of view and selectively uses data only to prove that one point of view and disregards or trivializes any comparable data to support a different view point. For example, lines 3-5, p. 3-13 implies that since "one third of marriages are contracted between persons living less than 10 miles apart" that this "propinquity of marriage partners contributes to ethnic endogamy". What then can be said about the fact that two-thirds of marriages are therefore contracted by persons living more than 10 miles apart?

I recognize full well that I am not an expert in the field of population genetics; but one doesn't have to be one to see that there are legitimate different points of view by such experts which are not sufficiently acknowledged in this chapter. I think the National Academy of Science should be concerned that any report issued under their auspices be scientifically accurate and balanced.

An area in which I do possess some expertise but which is also ignored in Chapter 3 relates to my previous and continuing objection to the statement on lines 7-11 on p. 3-30. As I stated in my response to the sign-off of the previous draft of this report, I cannot allow my name to be associated with a report that make such an irresponsible statement - nor should the National Academy of Science. I reiterate here my objections to this

statement for the reasons I articulated in my letter of May 23, 1991.

I am as anxious as the Academy to see this report issued and do not wish to be the reason for further delay. However, the potential impact of this report on the criminal justice system and upon the reputation of the National Academy of Science is too great to sacrifice quality for expediency. I'm not sure how to resolve this issue and if I'm the only member who feels this strongly about Chapter 3. From discussions with George Sensabaugh and Tom Caskey (and his recent writings on the subject), I would anticipate they share my concerns; but I cannot and do not speak for them.

For me to sign-off on Chapter 3, would not require a major re-write; just a modification of those statements which essentially limit the reporting of statistical inclusion to the method of empirical counting. Rather, given the considerable body of evidence to suggest that many experts believe the use of the multiplication rule appropriate, recommend the interim use of the multiplication method in conjunction with a 10% ceiling frequency until the suggested sub-population study results in a more empirically derived number. In this manner the likelihood of a match occurring at 4 loci (with 8 alleles) would be reported at a maximum of 1: 6,250,000.

This approach would be more consistent and balanced with the general assertions of this chapter and specifically lines 1-4 of p. 3-21 which state:

"The multiplication rule will yield valid and conservative estimates even for a substructured population provided that the allele frequencies used in the calculation exceed the allele frequencies in any of the population subgroups."

and with lines 9-18, p. 3-24;

"we selected [10%] by reasoning that the allele frequency employed in the calculations should be considerably greater than the typical fluctuations caused by genetic draft..."

I think the changes suggested herein will improve significantly the responsiveness of this report to the concerns of the reviewers and several members of the committee itself.

I remain available to discuss this issue in the coming days or weeks should you decide that to be appropriate.

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